

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2004, 06:34:09 ; Search time 176 Seconds  
(without alignments)  
3593.145 Million cell updates/sec

Title: US-09-783-436A-14  
Perfect score: 3697  
Sequence: 1 MLPRGRPRALGAAALLLLLLL.....GAAALKYLPALQQPQSPARG 695

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/2/paa/PCTUS\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep:\*
- 7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep:\*
- 8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep:\*
- 9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep:\*
- 10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep:\*
- 11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep:\*
- 12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep:\*
- 13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep:\*
- 14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep:\*
- 15: /cgn2\_6/ptodata/2/paa/US091\_COMB.pep:\*
- 16: /cgn2\_6/ptodata/2/paa/US092\_COMB.pep:\*
- 17: /cgn2\_6/ptodata/2/paa/US093\_COMB.pep:\*
- 18: /cgn2\_6/ptodata/2/paa/US094\_COMB.pep:\*
- 19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep:\*
- 20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep:\*
- 21: /cgn2\_6/ptodata/2/paa/US097A\_COMB.pep:\*
- 22: /cgn2\_6/ptodata/2/paa/US097B\_COMB.pep:\*
- 23: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep:\*
- 24: /cgn2\_6/ptodata/2/paa/US099A\_COMB.pep:\*
- 25: /cgn2\_6/ptodata/2/paa/US099B\_COMB.pep:\*
- 26: /cgn2\_6/ptodata/2/paa/US100\_COMB.pep:\*
- 27: /cgn2\_6/ptodata/2/paa/US101\_COMB.pep:\*

28: /cgn2\_6/ptodata/2/paa/US102\_COMB.pep:\*  
 29: /cgn2\_6/ptodata/2/paa/US103\_COMB.pep:\*  
 30: /cgn2\_6/ptodata/2/paa/US104\_COMB.pep:\*  
 31: /cgn2\_6/ptodata/2/paa/US106\_COMB.pep:\*  
 32: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3697	100.0	695	1	PCT-US03-03401-150	Sequence 150, App
2	3697	100.0	695	1	PCT-US03-03401A-150	Sequence 150, App
3	3697	100.0	695	22	US-09-783-436-14	Sequence 14, Appl
4	3697	100.0	695	22	US-09-783-436-74	Sequence 74, Appl
5	3697	100.0	695	22	US-09-783-436A-14	Sequence 14, Appl
6	3697	100.0	695	22	US-09-783-436A-74	Sequence 74, Appl
7	3697	100.0	695	25	US-09-970-813A-14	Sequence 14, Appl
8	3697	100.0	695	25	US-09-970-813A-74	Sequence 74, Appl
9	3530	95.5	721	1	PCT-US02-37431-67	Sequence 67, Appl
10	3530	95.5	721	28	US-10-214-831-2	Sequence 2, Appli
11	3530	95.5	721	28	US-10-288-252-14	Sequence 14, Appl
12	3530	95.5	721	29	US-10-301-822-67	Sequence 67, Appl
13	3530	95.5	721	32	US-60-311-150-2	Sequence 2, Appli
14	3526	95.4	721	27	US-10-108-260A-3470	Sequence 3470, Ap
15	3517	95.1	721	1	PCT-US03-03401-140	Sequence 140, App
16	3517	95.1	721	1	PCT-US03-03401A-140	Sequence 140, App
17	3511.5	95.0	690	1	PCT-US03-03401-134	Sequence 134, App
18	3511.5	95.0	690	1	PCT-US03-03401-154	Sequence 154, App
19	3511.5	95.0	690	1	PCT-US03-03401A-134	Sequence 134, App
20	3511.5	95.0	690	1	PCT-US03-03401A-154	Sequence 154, App
21	3511.5	95.0	690	28	US-10-288-252-16	Sequence 16, Appl
22	3511.5	95.0	695	1	PCT-US03-03401-144	Sequence 144, App
23	3511.5	95.0	695	1	PCT-US03-03401A-144	Sequence 144, App
24	3511.5	95.0	696	1	PCT-US03-03401-152	Sequence 152, App
25	3511.5	95.0	696	1	PCT-US03-03401A-152	Sequence 152, App
26	3503.5	94.8	690	1	PCT-US03-03401-142	Sequence 142, App
27	3503.5	94.8	690	1	PCT-US03-03401A-142	Sequence 142, App
28	3503.5	94.8	690	26	US-10-094-749-2231	Sequence 2231, Ap
29	3360	90.9	642	1	PCT-US03-03401-148	Sequence 148, App
30	3360	90.9	642	1	PCT-US03-03401A-148	Sequence 148, App
31	3360	90.9	642	22	US-09-783-436-73	Sequence 73, Appl
32	3360	90.9	642	22	US-09-783-436A-73	Sequence 73, Appl
33	3360	90.9	642	25	US-09-970-813A-73	Sequence 73, Appl
34	3357	90.8	781	1	PCT-US03-03401-136	Sequence 136, App
35	3357	90.8	781	1	PCT-US03-03401A-136	Sequence 136, App
36	3309	89.5	619	22	US-09-783-436-47	Sequence 47, Appl
37	3309	89.5	619	25	US-09-970-813A-47	Sequence 47, Appl
38	3299.5	89.2	738	1	PCT-US03-03401-138	Sequence 138, App
39	3299.5	89.2	738	1	PCT-US03-03401A-138	Sequence 138, App
40	3186	86.2	617	1	PCT-US03-03401-146	Sequence 146, App
41	3186	86.2	617	1	PCT-US03-03401A-146	Sequence 146, App
42	3186	86.2	617	22	US-09-783-436A-6	Sequence 6, Appli

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OM protein - protein search, using sw model

Run on: February 14, 2004, 06:35:04 ; Search time 23 Seconds  
(without alignments)  
2378.108 Million cell updates/sec

Title: US-09-783-436A-14  
Perfect score: 3697  
Sequence: 1 MLPRGRPRALGAAALLLLLL.....GAAALKYLPALQQPQSPARG 695

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 378584 seqs, 78699973 residues

Total number of hits satisfying chosen parameters: 378584

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	3697	100.0	695	6	US-10-357-885-150	Sequence 150, App
2	3517	95.1	721	6	US-10-357-885-140	Sequence 140, App
3	3511.5	95.0	690	6	US-10-357-885-134	Sequence 134, App
4	3511.5	95.0	690	6	US-10-357-885-154	Sequence 154, App
5	3511.5	95.0	695	6	US-10-357-885-144	Sequence 144, App
6	3511.5	95.0	696	6	US-10-357-885-152	Sequence 152, App
7	3503.5	94.8	690	6	US-10-357-885-142	Sequence 142, App
8	3360	90.9	642	6	US-10-357-885-148	Sequence 148, App
9	3357	90.8	781	6	US-10-357-885-136	Sequence 136, App
10	3299.5	89.2	738	6	US-10-357-885-138	Sequence 138, App

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OM protein - protein search, using sw model

Run on: February 14, 2004, 06:16:59 ; Search time 41 Seconds  
(without alignments)  
4374.306 Million cell updates/sec

Title: US-09-783-436A-14  
Perfect score: 3697  
Sequence: 1 MLPRGRPRALGAAALLLLLL.....GAAALKYLPALQQPQSPARG 695

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp Vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3530	95.5	721	4	Q8N3Y3	Q8n3y3 homo sapien
2	3526	95.4	721	4	Q8N8Y6	glycosyl-family 8 Q8n8y6 homo sapien
3	2810	76.0	629	11	Q8BJZ8	Q8bjz8 <u>mus</u> musculu
4	1353	36.6	285	11	Q8K253	Q8k253 <u>mus</u> musculu
5	1290	34.9	274	4	Q8NAK3	Q8nak3 homo sapien
6	908	24.6	622	5	Q21389	family 8 Q21389 caenorhabdi
7	893.5	24.2	257	4	Q8WY62	fragment-inhibit cance Q8wy62 homo sapien
8	322	8.7	1318	5	Q8MMX3	Q8mmx3 dictyosteli
9	299.5	8.1	415	11	Q8BWP8	Q8bwp8 mus musculu
10	260	7.0	379	11	Q8BJH9	Q8bjh9 mus musculu
11	251	6.8	379	11	Q8K2I0	Q8k2i0 mus musculu
12	251	6.8	389	5	Q9W1A7	Q9w1a7 drosophila
13	247.5	6.7	118	11	Q8BHM3	Q8bhm3 mus musculu
14	247	6.7	241	11	Q99LW7	Q99lw7 mus musculu
15	246	6.7	393	4	Q8NBI6	Q8nbi6 homo sapien
16	241.5	6.5	380	4	Q8WV03	Q8wv03 homo sapien
17	230	6.2	458	5	Q9W1D1	Q9w1d1 drosophila
18	229	6.2	458	5	Q95SJ1	Q95sj1 drosophila
19	222	6.0	328	5	Q9VBY3	Q9vby3 drosophila
20	195	5.3	409	4	Q8IXV1	Q8ixv1 homo sapien
21	177	4.8	544	5	Q9VMM5	Q9vmm5 drosophila
22	176.5	4.8	190	4	Q96ME0	Q96me0 homo sapien
23	171	4.6	407	5	Q9VK55	Q9vk55 drosophila
24	148.5	4.0	341	5	O61921	O61921 caenorhabdi
25	143	3.9	346	10	O04253	O04253 arabidopsis
26	142	3.8	346	10	Q8LD72	Q8ld72 arabidopsis
27	141.5	3.8	353	10	Q9FQZ3	Q9fqz3 nicotiana t
28	140.5	3.8	367	16	O25962	O25962 helicobacte
29	137	3.7	349	5	O02230	O02230 caenorhabdi
30	135.5	3.7	649	10	Q8H4X4	Q8h4x4 oryza sativ
31	133.5	3.6	313	10	Q8RX31	Q8rx31 arabidopsis
32	132.5	3.6	1681	5	Q8T1G8	Q8tlg8 dictyosteli
33	130	3.5	365	10	Q9LHD2	Q9lhd2 arabidopsis
34	128.5	3.5	377	10	Q8LIF5	Q8lif5 oryza sativ
35	128.5	3.5	417	5	O18090	O18090 caenorhabdi
36	128	3.5	367	16	Q9ZJJ6	Q9zjj6 helicobacte
37	128	3.5	1493	5	Q9GPA0	Q9gpa0 caenorhabdi
38	127.5	3.4	510	10	Q9MAB8	Q9mab8 arabidopsis
39	126	3.4	1548	5	Q9VVT7	Q9vvt7 drosophila
40	125.5	3.4	373	16	Q9ZKW4	Q9zkw4 helicobacte
41	125.5	3.4	390	10	O04536	O04536 arabidopsis
42	125.5	3.4	1377	5	P91854	P91854 caenorhabdi
43	125	3.4	187	4	Q8NAL3	Q8nal3 homo sapien
44	124	3.4	302	16	Q9CLS0	Q9cls0 pasteurilla
45	122	3.3	357	10	Q9LZJ9	Q9lzej9 arabidopsis

## ALIGNMENTS

RESULT 1  
Q8N3Y3

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OM protein - protein search, using sw model

Run on: February 14, 2004, 06:13:53 ; Search time 47 Seconds  
(without alignments)  
2347.127 Million cell updates/sec

Title: US-09-783-436A-14  
Perfect score: 3697  
Sequence: 1 MLPRGRPRALGAAALLLLLL.....GAAALKYLPALQQPQSPARG 695

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_19Jun03:\*  
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*  
2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*  
3: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\*  
4: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:\*  
5: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:\*  
6: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:\*  
7: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:\*  
8: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:\*  
9: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:\*  
10: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:\*  
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12: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:\*  
13: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:\*  
14: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:\*  
15: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:\*  
16: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1995.DAT:\*  
17: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:\*  
18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:\*  
19: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:\*  
20: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:\*  
21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	3697	100.0	695	22	AAE08926		Human NOVX7 protei
2	3530	95.5	721	23	AAE22152	human transferases	Human TRNFR-14 pro
3	3511.5	95.0	690	23	AAE22154		Human TRNFR-16 pro
4	3360	90.9	642	22	AAE08927		Human NOVX7 protei
5	3185.5	86.2	616	22	AAE08922		Human NOVX3 protei
6	2407.5	65.1	756	19	AAW74724		Human secreted pro
7	2407.5	65.1	756	23	ABP61839		Human polypeptide
8	2407.5	65.1	785	22	ABG05481		Novel human diagno
9	2292.5	62.0	793	22	ABG05479		Novel human diagno
10	2288	61.9	692	22	ABG05480		Novel human diagno
11	1945	52.6	368	21	AAB42092		Human ORFX ORF1856
12	1002.5	27.1	255	23	ABB72401		Murine protein iso
13	908	24.6	622	22	AAB50679		C. elegans I-beta-
14	893.5	24.2	257	23	ABB06786		Human cancer cell
15	348	9.4	87	22	ABB15409		Human nervous syst
16	290.5	7.9	415	20	AAY28355		Beta 1,3-N-acetylgl
17	290.5	7.9	415	22	AAB50671		Human i-beta-1,3-N
18	251	6.8	389	22	ABB59758		Drosophila melanog
19	246	6.7	393	22	AAB88481		Human membrane or
20	241.5	6.5	380	22	AAE03835		Human gene 18 enco
21	241.5	6.5	380	23	ABG64570		Human albumin fusi
22	230	6.2	458	22	ABB65700		Drosophila melanog
23	222	6.0	328	22	ABB64815		Drosophila melanog
24	215	5.8	65	22	ABB31283		Peptide #3934 enco
25	215	5.8	65	22	ABB21831		Protein #3830 enco
26	215	5.8	65	22	AAM57252		Human brain expres
27	196.5	5.3	368	24	ABU11485		Human MDDT polypep
28	177	4.8	608	22	ABB64278		Drosophila melanog
29	171	4.6	407	22	ABB70686		Drosophila melanog
30	148.5	4.0	341	22	AAB50678		C. elegans I-beta-
31	145	3.9	41	22	ABG05482		Novel human diagno
32	143	3.9	332	21	AAG45491		Arabidopsis thalia
33	143	3.9	346	21	AAG45490		Arabidopsis thalia
34	143	3.9	346	23	ABB92808		Herbicidally activ
35	142	3.8	332	21	AAG15767		Arabidopsis thalia
36	142	3.8	346	21	AAG15766		Arabidopsis thalia
37	137	3.7	349	22	AAB50681		C. elegans I-beta-
38	135.5	3.7	121	22	AAB50672		Human partial i-be
39	130	3.5	323	21	AAG10403		Arabidopsis thalia
40	130	3.5	364	21	AAG10402		Arabidopsis thalia
41	130	3.5	365	21	AAG10401		Arabidopsis thalia
42	129	3.5	323	21	AAG15508		Arabidopsis thalia
43	129	3.5	364	21	AAG15507		Arabidopsis thalia
44	129	3.5	365	21	AAG15506		Arabidopsis thalia
45	128.5	3.5	417	22	AAB50680		C. elegans I-beta-

# ALIGNMENTS

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OM protein - protein search, using sw model

Run on: February 14, 2004, 06:33:39 ; Search time 22 Seconds  
(without alignments)  
1336.638 Million cell updates/sec

Title: US-09-783-436A-14  
Perfect score: 3697  
Sequence: 1 MLPRGRPRALGAAALLLLLL.....GAAALKYLPALQQPQSPARG 695

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	290.5	7.9	415	4	US-09-182-450-1	Sequence 1, Appli
2	128	3.5	1493	4	US-09-376-330-16	Sequence 16, Appl
3	126	3.4	1548	4	US-09-376-330-15	Sequence 15, Appl
4	116.5	3.2	1447	4	US-09-376-330-17	Sequence 17, Appl
5	116	3.1	2628	3	US-09-413-814-11	Sequence 11, Appl
6	105.5	2.9	769	4	US-09-252-991A-19611	Sequence 19611, A
7	103.5	2.8	581	4	US-09-252-991A-30032	Sequence 30032, A
8	101	2.7	775	4	US-09-996-243-326	Sequence 326, App
9	100	2.7	371	4	US-09-996-243-171	Sequence 171, App
10	99.5	2.7	719	4	US-09-252-991A-22278	Sequence 22278, A
11	99.5	2.7	856	4	US-09-252-991A-24761	Sequence 24761, A



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OM protein - protein search, using sw model

Run on: February 14, 2004, 06:35:34 ; Search time 39 Seconds  
(without alignments)  
3731.300 Million cell updates/sec

Title: US-09-783-436A-14  
Perfect score: 3697  
Sequence: 1 MLPRGRPRALGAAALLLLLL.....GAAALKYLPALQQPQSPARG 695

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3530	95.5	721	12	US-10-288-252-14	Sequence 14, Appl
2	3530	95.5	721	12	US-10-301-822-67	Sequence 67, Appl
3	3526	95.4	721	12	US-10-108-260A-3470	Sequence 3470, Ap
4	3511.5	95.0	690	12	US-10-288-252-16	Sequence 16, Appl
5	3503.5	94.8	690	12	US-10-094-749-2231	Sequence 2231, Ap
6	2407.5	65.1	756	9	US-09-745-763-142	Sequence 142, App
7	1290	34.9	274	12	US-10-104-047-3079	Sequence 3079, Ap
8	1002.5	27.1	255	11	US-09-866-050A-725	Sequence 725, App
9	290.5	7.9	415	12	US-10-166-098-1	Sequence 1, Appli
10	241.5	6.5	380	12	US-09-833-245-1319	Sequence 1319, Ap
11	215	5.8	65	9	US-09-864-761-37129	Sequence 37129, A
12	176.5	4.8	190	12	US-10-094-749-2918	Sequence 2918, Ap
13	126	3.4	1548	12	US-10-161-051-74	Sequence 74, Appl
14	125	3.4	187	12	US-10-104-047-3057	Sequence 3057, Ap
15	118.5	3.2	334	16	US-10-176-306-38	Sequence 38, Appl
16	115	3.1	1267	12	US-09-769-734-38	Sequence 38, Appl
17	110	3.0	827	12	US-10-347-470A-16	Sequence 16, Appl
18	103	2.8	718	15	US-10-142-143-20	Sequence 20, Appl
19	103	2.8	3192	12	US-10-132-134-10	Sequence 10, Appl
20	102.5	2.8	1045	15	US-10-156-761-13486	Sequence 13486, A
21	101.5	2.7	830	12	US-10-369-493-21037	Sequence 21037, A
22	101	2.7	775	9	US-09-989-722-326	Sequence 326, App
23	101	2.7	775	9	US-09-989-723-326	Sequence 326, App
24	101	2.7	775	9	US-09-989-279-326	Sequence 326, App
25	101	2.7	775	9	US-09-989-727-326	Sequence 326, App
26	101	2.7	775	10	US-09-989-731-326	Sequence 326, App
27	101	2.7	775	10	US-09-989-732-326	Sequence 326, App
28	101	2.7	775	10	US-09-991-073-326	Sequence 326, App
29	101	2.7	775	10	US-09-990-442-326	Sequence 326, App
30	101	2.7	775	10	US-09-991-163-326	Sequence 326, App
31	101	2.7	775	10	US-09-993-604-326	Sequence 326, App
32	101	2.7	775	10	US-09-990-456-326	Sequence 326, App
33	101	2.7	775	10	US-09-989-721-326	Sequence 326, App
34	101	2.7	775	10	US-09-992-598-326	Sequence 326, App
35	101	2.7	775	10	US-09-989-293A-326	Sequence 326, App
36	101	2.7	775	10	US-09-989-735-326	Sequence 326, App
37	101	2.7	775	10	US-09-990-444-326	Sequence 326, App
38	101	2.7	775	10	US-09-991-181-326	Sequence 326, App
39	101	2.7	775	10	US-09-989-730-326	Sequence 326, App
40	101	2.7	775	10	US-09-990-436-326	Sequence 326, App
41	101	2.7	775	10	US-09-993-687-326	Sequence 326, App
42	101	2.7	775	11	US-09-989-734-326	Sequence 326, App
43	101	2.7	775	11	US-09-997-653-326	Sequence 326, App
44	101	2.7	775	11	US-09-993-667-326	Sequence 326, App
45	101	2.7	775	11	US-09-997-428-326	Sequence 326, App

## ALIGNMENTS

RESULT 1  
US-10-288-252-14

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OM protein - protein search, using sw model

Run on: February 14, 2004, 06:29:54 ; Search time 21 Seconds  
(without alignments)  
3182.725 Million cell updates/sec

Title: US-09-783-436A-14  
Perfect score: 3697  
Sequence: 1 MLPRGRPRALGAAALLLLLL.....GAAALKYLPALQQPQSPARG 695

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2293	62.0	693	2	T00256		hypothetical prote
2	908	24.6	622	2	T23541		hypothetical prote
3	148.5	4.0	341	2	T33252		hypothetical prote
4	143	3.9	346	2	T01514		glycosyl transfera
5	140.5	3.8	367	2	H64696		lipopolysaccharide
6	137	3.7	349	2	T20202		hypothetical prote
7	128.5	3.5	417	2	T21226		hypothetical prote
8	128	3.5	367	2	H71822		lipopolysaccharide
9	128	3.5	1493	2	T16404		hypothetical prote
10	126	3.4	1548	2	S54723		UDP-glucose-glycop
11	125.5	3.4	373	2	F71884		probable lipopolys
12	125.5	3.4	390	2	F96723		hypothetical prote
13	125.5	3.4	1377	2	T19214		UDP-glucose-glycop

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OM protein - protein search, using sw model

Run on: February 14, 2004, 06:15:18 ; Search time 17 Seconds  
(without alignments)  
1922.562 Million cell updates/sec

Title: US-09-783-436A-14  
Perfect score: 3697  
Sequence: 1 MLPRGRPRALGAAALLLLLL.....GAAALKYLPALQQPQSPARG 695

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2407.5	65.1	756	1	LAGE_HUMAN	O95461	homo sapien
2	2406.5	65.1	756	1	LAGE_MOUSE	Q9zlm7	mus musculu
3	290.5	7.9	415	1	B3G6_HUMAN	O43505	h n-acetyll
4	126	3.4	1548	1	UGGG_DROME	Q09332	drosophila
5	124	3.4	1448	1	UGGG_SCHPO	Q09140	schizosacch
6	122.5	3.3	902	1	NRFI_WOLSU	Q9sle4	wolinella s
7	114.5	3.1	1126	1	HPS5_MOUSE	P59438	mus musculu
8	110.5	3.0	286	1	GSPA_BACSU	P25148	bacillus su
9	110	3.0	4684	1	PLE1_HUMAN	Q15149	homo sapien
10	108.5	2.9	506	1	MATK_RHOSC	Q8mff0	rhodotypos
11	108.5	2.9	559	1	QUA1_ARATH	Q9lsg3	arabidopsis
12	106	2.9	503	1	MATK_PURTR	Q8wjn9	purshia tri
13	106	2.9	976	1	VP41_ARATH	P93043	arabidopsis
14	104.5	2.8	1094	1	EX5B_MYCTU	P96920	mycobacteri
15	104	2.8	1159	1	SOR2_HUMAN	Q96pq0	homo sapien
16	103.5	2.8	1874	1	POLR_KYMVJ	P36304	kennedya ye
17	103	2.8	718	1	EXT2_MOUSE	P70428	mus musculu